

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Herrmann, Stephen H.
Lu, Zhijian
McCoy, John M.
Swanberg, Stephen L.
Walker, Bruce
Yang, Otto

(ii) TITLE OF INVENTION: CHEMOKINES WITH AMINO-TERMINAL MODIFICATIONS

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 41,323

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Asn	Ala	Lys	Val	Val	Val	Val	Leu	Val	Leu	Val	Leu	Thr	Ala	Leu
1				5				10						15	
Cys	Leu	Ser	Asp	Gly	Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro	Cys
			20					25					30		
Arg	Phe	Phe	Glu	Ser	His	Val	Ala	Arg	Ala	Asn	Val	Lys	His	Leu	Lys
		35					40					45			
Ile	Leu	Asn	Thr	Pro	Asn	Cys	Ala	Leu	Gln	Ile	Val	Ala	Arg	Leu	Lys
	50					55					60				
Asn	Asn	Asn	Arg	Gln	Val	Cys	Ile	Asp	Pro	Lys	Leu	Lys	Trp	Ile	Gln
65					70					75					80
Glu	Tyr	Leu	Glu	Lys	Ala	Leu	Asn	Lys							
						85									

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asn	Ala	Lys	Val	Val	Val	Val	Leu	Val	Leu	Val	Leu	Thr	Ala	Leu
1				5				10						15	
Cys	Leu	Ser	Asp	Gly	Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro	Cys
			20					25					30		
Arg	Phe	Phe	Glu	Ser	His	Val	Ala	Arg	Ala	Asn	Val	Lys	His	Leu	Lys
		35					40					45			
Ile	Leu	Asn	Thr	Pro	Asn	Cys	Ala	Leu	Gln	Ile	Val	Ala	Arg	Leu	Lys
	50					55					60				
Asn	Asn	Asn	Arg	Gln	Val	Cys	Ile	Asp	Pro	Lys	Leu	Lys	Trp	Ile	Gln
65					70					75					80
Glu	Tyr	Leu	Glu	Lys	Ala	Leu	Asn	Lys	Arg	Phe	Lys	Met			
						85					90				

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1856 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCTCCGTCAG CCGCATTGCC CGCTCGGCGT CCGGCCCCCG ACCCGTGCTC GTCCGCCCCG	60
CCGCCCCGCC GCGCGCGCCA TGAACGCCAA GGTCTGGTCC GTGCTGGTCC TCGTGCTGAC	120
CGCGCTCTGC CTCAGCGACG GGAAGCCCCG CAGCCTGAGC TACAGATGCC CATGCCGATT	180
CTTCGAAAAGC CATGTTGCCA GAGCCAACGT CAAGCATCTC AAAATTCTCA ACACTCCAAA	240
CTGTGCCCTT CAGATTGTAG CCCGGCTGAA GAACAACAAC AGACAAGTGT GCATTGACCC	300
GAAGCTAAAG TGGATTTCAGG AGTACCTGGA GAAAGCTTTA AACAAGTAAG CACAACAGCC	360
AAAAAGGACT TTCCGCTAGA CCCACTCGAG GAAACTAAA ACCTTGTTGAG AGATGAAAGG	420
GCAAAGACGT GGGGGAGGGG GCCTTAACCA TGAGGACCAG GTGTGTGTGT GGGGTGGGCA	480
CATTGATCTG GGATCGGGCC TGAGGTTTGC AGCATTTAGA CCCTGCATTT ATAGCATACG	540
GTATGATATT GCAGCTTATA TTCATCCATG CCCTGTACCT GTGCACGTTG GAACTTTTAT	600
TACTGGGGTT TTTCTTAGAA AGAAATTGTA TTATCAACAG CATTTTCAAG CAGTTAGTTC	660
CTTCATGATC ATCACAATCA TCATCATCTT CATTCTCATT TTTTAAATCA ACGAGTACTT	720
CAAGATCTGA ATTTGGCTTG TTTGGAGCAT CTCTCTGCT CCCCTGGGGA GTCTGGGCAC	780
AGTCAGGTGG TGGCTTAACA GGGAGCTGGA AAAAGTGTCC TTTCTTCAGA CACTGAGGCT	840
CCCGCAGCAG CGCCCCCTCCC AAGAGGAAGG CCTCTGTGGC ACTCAGATAC CGACTGGGGC	900
TGGGGCGCCG CCACTGCCTT CACCTCCTCT TTCAAACCTC AGTGATTGGC TCTGTGGGCT	960
CCATGTAGAA GCCACTATTA CTGGGACTGT CTCAGAGACC CCTCTCCCAG CTATTCCTAC	1020
TCTCTCCCCG ACTCCGAGAG CATGCTTAAT CTTGCTTCTG CTTCTCATTT CTGTAGCCTG	1080
ATCAGCGCCG CACCAGCCGG GAAGAGGGTG ATTGCTGGGG CTCGTGCCCT GCATCCCTCT	1140
CCTCCCAGGG CCTGCCCCAC AGCTCGGGCC CTCTGTGAGA TCCGTCTTTG GCCTCCTCCA	1200

GAATGGAGCT	GGCCCTCTCC	TGGGGATGTG	TAATGGTCCC	CCTGCTTACC	CGCAAAAGAC	1260
AAGTCTTTAC	AGAATCAAAT	GCAATTTTAA	ATCTGAGAGC	TCGCTTGAGT	GACTGGGTTT	1320
GTGATTGCCT	CTGAAGCCTA	TGTATGCCAT	GGAGGCACTA	ACAAACTCTG	AGGTTTCCGA	1380
AATCAGAAGC	GAAAAAATCA	GTGAATAAAC	CATCATCTTG	CCACTACCCC	CTCCTGAAGC	1440
CACAGCAGGG	GTTCAGGTTC	CAATCAGAAC	TGTTGGCAAG	GTGACATTTT	CATGCATAGA	1500
TGCGATCCAC	AGAAGGTCCT	GGTGGTATTT	GTAACITTTTT	GCAAGGCATT	TTTTTATATA	1560
TATTTTTGTG	CACATTTTTT	TTTACGATTC	TTTAGAAAAC	AAATGTATTT	CAAAATATAT	1620
TTATAGTCGA	ACAAGTCATA	TATATGAATG	AGAGCCATAT	GAATGTCAGT	AGTTTATACT	1680
TCTCTATTAT	CTCAAACCTAC	TGGCAATTTG	TAAAGAAATA	TATATGATAT	ATAAATGTGA	1740
TTGCAGCTTT	TCAATGTTAG	CCACAGTGTA	TTTTTTCACT	TGTACTAAAA	TTGTATCAAA	1800
TGTGACATTA	TATGCACTAG	CAATAAAATG	CTAATTGTTT	CATGGTAAAA	AAAAAA	1856

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCTCCGTCAG	CCGCATTGCC	CGCTCGGCGT	CCGGCCCCCG	ACCCGTGCTC	GTCCGCCCGC	60
CCGCCCCGCC	GCCCGCGCCA	TGAACGCCAA	GGTCGTGGTC	GTGCTGGTCC	TCGTGCTGAC	120
CGCGCTCTGC	CTCAGCGACG	GGAAGCCCGT	CAGCCTGAGC	TACAGATGCC	CATGCCGATT	180
CTTCGAAAGC	CATGTTGCCA	GAGCCAACGT	CAAGCATCTC	AAAATTCTCA	ACACTCCAAA	240
CTGTGCCCTT	CAGATTGTAG	CCCGGCTGAA	GAACAACAAC	AGACAAGTGT	GCATTGACCC	300
GAAGCTAAAG	TGGATTCAGG	AGTACCTGGA	GAAAGCTTTA	AACAAGAGGT	TCAAGATGTG	360
AGAGGGTCAC	ACGCCTGAGG	AACCCTTACA	GTAGGAGCCC	AGCTCTGAAA	CCAGTGTTAG	420
GGAAGGGCCT	GCCACAGCCT	CCCCTGCCAG	GGCAGCGCCC	CAGGCATTGC	CAAGGGCTTT	480
GTTTTGCACA	CTTTGCCATA	TTTTCACCAT	TTGATTATGT	AGCAAAATAC	ATGACATTTA	540

TTTTTCATTT	AGTTTGATTA	TTCAGTGTCA	CTGGCGACAC	GTAGCAGCTT	AGACTAAGGC	600
CATTATTGTA	CTTGCCTTAT	TAGAGTGTCT	TTCCACGGAG	CCACTCCTCT	GACTCAGGGC	660
TCCTGGGTTT	TGTATTCTCT	GAGCTGTGCA	GGTGGGGAGA	CTGGGCTGAG	GGAGCCTGGC	720
CCCATGGTCA	GCCCTAGGGT	GGAGAGCCAC	CAAGAGGGAC	GCCTGGGGGT	GCCAGGACCA	780
GTCAACCTGG	GCAAAGCCTA	GTGAAGGCTT	CTCTCTGTGG	GATGGGATGG	TGGAGGGCCA	840
CATGGGAGGC	TCACCCCCTT	CTCCATCCAC	ATGGGAGCCG	GGTCTGCCCT	TTCCTGGGAGG	900
GCAGCAGGGC	TACCCCTGAGC	TGAGGCAGCA	GTGTGAGGCC	AGGGCAGAGT	GAGACCCAGC	960
CCTCATCCCG	AGCACCTCCA	CATCCTCCAC	GTTCTGCTCA	TCATTCTCTG	TCTCATCCAT	1020
CATCATGTGT	GTCCACGACT	GTCTCCATGG	CCCCGCAAAA	GGACTCTCAG	GACCAAAGCT	1080
TTCATGTAAA	CTGTGCACCA	AGCAGGAAAT	GAAAATGTCT	TGTGTTACCT	GAAAACACTG	1140
TGCACATCTG	TGTCTTGTGT	GGAATATTGT	CCATTGTCCA	ATCCTATGTT	TTTGTTCAAA	1200
GCCAGCGTCC	TCCTCTGTGA	CCAATGTCTT	GATGCATGCA	CTGTTCCCCC	TGTGCAGCCG	1260
CTGAGCGAGG	AGATGCTCCT	TGGGCCCTTT	GAGTGCAGTC	CTGATCAGAG	CCGTGGTCCT	1320
TTGGGGTGAA	CTACCTTGGT	TCCCCACTG	ATCACAAAAA	CATGGTGGGT	CCATGGGCAG	1380
AGCCCAAGGG	AATTCGGTGT	GCACCAGGGT	TGACCCAGAG	GGATTGCTGC	CCCATCAGTG	1440
CTCCCTCACA	TGTCAGTACC	TTCAAAC TAG	GGCCAAGCCC	AGCACTGCTT	GAGGAAAACA	1500
AGCATTCACA	ACTTGTTTTT	GGTTTTTTAAA	ACCCAGTCCA	CAAAATAACC	AATCCTGGAC	1560
ATGAAGATTC	TTTCCCAATT	CACATCTAAC	CTCATCTTCT	TCACCATTTG	GCAATGCCAT	1620
CATCTCCTGC	CTTCCTCCTG	GGCCCTCTCT	GCTCTGCGTG	TCACCTGTGC	TTCGGGCCCT	1680
TCCCACAGGA	CATTTCTCTA	AGAGAACAAT	GTGCTATGTG	AAGAGTAAGT	CAACCTGCCT	1740
GACATTGGA	GTGTTCCCCC	CCCCTGAGG	GCAGTCGATA	GAGCTGTATT	AAGCCACTTA	1800
AAATGTTTAC	TTTTGACAAA	GGCAAGCACT	TGTGGGTTTT	TGTTTTGT	TTCATTTCAGT	1860
CTTACGAATA	CTTTTGCCCT	TTGATTAAAG	ACTCCAGTTA	AAAAAAATTT	TAATGAAGAA	1920
AGTGGAAGAA	AAGGAAGTCA	AAGCAAGGAA	ACTATGTAAC	ATGTAGGAAG	TAGGAAGTAA	1980
ATTATAGTGA	TGTAATCTTG	AATTGTAAC	GTTTCGTGAAT	TTAATAATCT	GTAGGGTAAT	2040
TAGTAACATG	TGTTAAGTAT	TTTCATAAGT	ATTTCAAATT	GGAGCTTCAT	GGCAGAAGGC	2100
AAACCCATCA	ACAAAAATTG	TCCCTTAAAC	AAAAATTAAA	ATCCTCAATC	CAGCTATGTT	2160
ATATTGAAAA	AATAGAGCCT	GAGGGATCTT	TACTAGTTAT	AAAGATACAG	AACTCTTTCA	2220

AAACCTTTTG	AAATTAACCT	CTCACTATAC	CAGTATAATT	GAGTTTTTCAG	TGGGGCAGTC	2280
ATTATCCAGG	TAATCCAAGA	TATTTTAAAA	TCTGTCACGT	AGAACTTGGA	TGTACCTGCC	2340
CCCAATCCAT	GAACCAAGAC	CATTGAATTC	TTGGTTGAGG	AAACAAACAT	GACCCATAAT	2400
CTTGACTACA	GTCAGGAAAG	GAATCATTTT	TATTTCTCCT	CCATGGGAGA	AAATAGATAA	2460
GAGTAGAAAC	TGCAGGGAAA	ATTATTTGCA	TAACAATTCC	TCTACTAACA	ATCAGCTCCT	2520
TCCTGGAGAC	TGCCCAGCTA	AAGCAATATG	CATTTAAATA	CAGTCTTCCA	TTTGCAAGGG	2580
AAAAGTCTCT	TGTAATCCGA	ATCTCTTTTT	GCTTTCGAAC	TGCTAGTCAA	GTGCGTCCAC	2640
GAGCTGTTTA	CTAGGGATCC	CTCATCTGTC	CCTCCGGGAC	CTGGTGCTGC	CTCTACCTGA	2700
CACTCCCTTG	GGCTCCCTGT	AACCTCTTCA	GAGGCCCTCG	CTGCCAGCTC	TGTATCAGGA	2760
CCCAGAGGAA	GGGGCCAGAG	GCTCGTTGAC	TGGCTGTGTG	TTGGGATTGA	GTCTGTGCCA	2820
CGTGATGTG	CTGTGGTGTG	TCCCCCTCTG	TCCAGGCACT	GAGATACCAG	CGAGGAGGCT	2880
CCAGAGGGCA	CTCTGCTTGT	TATTAGAGAT	TACCTCCTGA	GAAAAAAGCT	TCCGCTTGGA	2940
GCAGAGGGGC	TGAATAGCAG	AAGGTTGCAC	CTCCCCAAC	CTTAGATGTT	CTAAGTCTTT	3000
CCATTGGATC	TCATTGGACC	CTTCCATGGT	GTGATCGTCT	GAAGTGGTGT	ATCACCGTGG	3060
GCTCCCTGAC	TGGGAGTTGA	TCGCCTTTCC	CAGGTGCTAC	ACCCTTTTCC	AGCTGGATGA	3120
GAATTTGAGT	GCTCTGATCC	CTCTACAGAG	CTTCCCTGAC	TCATTCTGAA	GGAGCCCCAT	3180
TCCTGGGAAA	TATTCCTTAG	AAACTTCCAA	ATCCCCTAAG	CAGACCACTG	ATAAAACCAT	3240
GTAGAAAATT	TGTTATTTTG	CAACCTCGCT	GGACTCTCAG	TCTCTGAGCA	GTGAATGATT	3300
CAGTGTTAAA	TGTGATGAAT	ACTGTATTTT	GTATTGTTTC	AAGTGCATCT	CCCAGATAAT	3360
GTGAAAATGG	TCCAGGAGAA	GGCCAATTCC	TATACGCAGC	GTGCTTTAAA	AAATAAATAA	3420
GAAACAACCT	TTTGAGAAAC	AACAATTCTT	ACTTTGAAGT	CATACCAATG	AAAAAATGTA	3480
TATGCACTTA	TAATTTTCCT	AATAAAGTTC	TGTACTCAAA	TGTAAA		3526

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ala Ala Lys Asp Val Lys His His His His His His Gly Ser Gly Ser
1 5 10 15
Asp Asp Asp Asp Lys
20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA construct"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGAAACCAG TATCTCTGTC TTATCGTTGT CCATGCCGAT TCTTCGAAAG CCATGTTGCC 60
AGAGCCAACG TCAAGCATCT CAAAATTCTC AACACTCCAA ACTGTGCCCT TCAGATTGTA 120
GCCCCGCTGA AGAACAACAA CAGACAAGTG TGCATTGACC CGAAGCTAAA GTGGATTTCAG 180
GAGTACCTGG AGAAAGCTTT AAACAAG 207

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA construct"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAAACCAG TATCTCTGTC TTATCGTTGT CCATGCCGAT TCTTCGAAAG CCATGTTGCC 60
AGAGCCAACG TCAAGCATCT CAAAATTCTC AACACTCCAA ACTGTGCCCT TCAGATTGTA 120
GCCCCGCTGA AGAACAACAA CAGACAAGTG TGCATTGACC CGAAGCTAAA GTGGATTTCAG 180

GAGTACCTGG AGAAAGCTTT AAACAAGCGT TTCAAATG

219

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA construct"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGGCAGCTA AAGACGTAAA ACATCACCAT CACCATCACG GTTCTGGTTC TGATGACGAT	60
GACAAAAAAC CAGTATCTCT GTCTTATCGT TGTCCATGCC GATTCTTCGA AAGCCATGTT	120
GCCAGAGCCA ACGTCAAGCA TCTCAAAATT CTCAACACTC CAAACTGTGC CCTTCAGATT	180
GTAGCCCGGC TGAAGAACAA CAACAGACAA GTGTGCATTG ACCCGAAGCT AAAGTGGATT	240
CAGGAGTACC TGGAGAAAGC TTAAACAAG	270

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA construct"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGCAGCTA AAGACGTAAA ACATCACCAT CACCATCACG GTTCTGGTTC TGATGACGAT	60
GACAAAAAAC CAGTATCTCT GTCTTATCGT TGTCCATGCC GATTCTTCGA AAGCCATGTT	120
GCCAGAGCCA ACGTCAAGCA TCTCAAAATT CTCAACACTC CAAACTGTGC CCTTCAGATT	180
GTAGCCCGGC TGAAGAACAA CAACAGACAA GTGTGCATTG ACCCGAAGCT AAAGTGGATT	240
CAGGAGTACC TGGAGAAAGC TTAAACAAG CGTTTCAAAA TG	282

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro	Cys	Arg	Phe	Phe	Glu
1				5					10					15	
Ser	His	Val	Ala	Arg	Ala	Asn	Val	Lys	His	Leu	Lys	Ile	Leu	Asn	Thr
			20					25					30		
Pro	Asn	Cys	Ala	Leu	Gln	Ile	Val	Ala	Arg	Leu	Lys	Asn	Asn	Asn	Arg
			35				40					45			
Gln	Val	Cys	Ile	Asp	Pro	Lys	Leu	Lys	Trp	Ile	Gln	Glu	Tyr	Leu	Glu
	50					55					60				
Lys	Ala	Leu	Asn	Lys											
65															

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro	Cys	Arg	Phe	Phe	Glu
1				5					10					15	
Ser	His	Val	Ala	Arg	Ala	Asn	Val	Lys	His	Leu	Lys	Ile	Leu	Asn	Thr
			20					25					30		
Pro	Asn	Cys	Ala	Leu	Gln	Ile	Val	Ala	Arg	Leu	Lys	Asn	Asn	Asn	Arg
			35				40					45			
Gln	Val	Cys	Ile	Asp	Pro	Lys	Leu	Lys	Trp	Ile	Gln	Glu	Tyr	Leu	Glu
	50					55					60				

Lys Ala Leu Asn Lys Arg Phe Lys Met
65 70

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Ala	Ala	Lys	Asp	Val	Lys	His	His	His	His	His	Gly	Ser	Gly	
1			5					10					15		
Ser	Asp	Asp	Asp	Asp	Lys	Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro
			20					25					30		
Cys	Arg	Phe	Phe	Glu	Ser	His	Val	Ala	Arg	Ala	Asn	Val	Lys	His	Leu
		35					40					45			
Lys	Ile	Leu	Asn	Thr	Pro	Asn	Cys	Ala	Leu	Gln	Ile	Val	Ala	Arg	Leu
	50					55					60				
Lys	Asn	Asn	Asn	Arg	Gln	Val	Cys	Ile	Asp	Pro	Lys	Leu	Lys	Trp	Ile
65				70						75				80	
Gln	Glu	Tyr	Leu	Glu	Lys	Ala	Leu	Asn	Lys						
			85						90						

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ala	Ala	Lys	Asp	Val	Lys	His	His	His	His	His	Gly	Ser	Gly	
1			5					10					15		
Ser	Asp	Asp	Asp	Asp	Lys	Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro

	20		25		30
Cys Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu					
35		40		45	
Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu					
50		55		60	
Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile					
65		70		75	80
Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met					
	85		90		

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser			
1	5	10	15
His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro			
	20	25	30
Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln			
	35	40	45
Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys			
	50	55	60
Ala Leu Asn Lys			
65			

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
1 5 10 15

His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro
20 25 30

Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln
35 40 45

Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
50 55 60

Ala Leu Asn Lys Arg Phe Lys Met
65 70